

Sequence Listing could not be accepted due to errors.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2010; month=3; day=17; hr=8; min=6; sec=56; ms=101;]

Reviewer Comments:

 $\langle 210 \rangle$ 1

<211> 971

<212> PRT

<213> human

 $\langle 400 \rangle$ 1

(sample of error in Sequence 1 below)

Met Leu Arg Arg Pro Ala Pro Ala Leu Ala Pro Ala Ala Arg Leu Leu

1 5 10 15

Leu Ala Gly Leu Leu Cys Gly Gly Gly Val Trp Ala Ala Arg Val Asn

20 25 30

The above lines are samples of an error appearing throughout Sequence 1: please remove the blank lines between the amino acid numbers and their respective amino acids. Amino acid numbers must appear directly below

their respective amino acids. Same error in Sequences 2 through 17.

Application No: 10577008 Version No: 3.0

Input Set:

Output Set:

```

Started:      2010-03-05 16:51:39.132
Finished:    2010-03-05 16:51:47.096
Elapsed:     0 hr(s) 0 min(s) 7 sec(s) 964 ms
Total Warnings: 17
Total Errors:  430
No. of SeqIDs Defined: 17
Actual SeqID Count: 17

```

[illegible]

Error code	Error Description
E 321	No. of Bases conflict, this line has no nucleotides SEQID (1)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (1)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (1)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (1)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (1)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (1)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (1)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (1)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (1)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (1)
E 355	Empty lines found between the amino acid numbering and the proteins
E 321	No. of Bases conflict, this line has no nucleotides SEQID (1) POS (304)

Input Set:

Output Set:

Started: 2010-03-05 16:51:39.132
Finished: 2010-03-05 16:51:47.096
Elapsed: 0 hr(s) 0 min(s) 7 sec(s) 964 ms
Total Warnings: 17
Total Errors: 430
No. of SeqIDs Defined: 17
Actual SeqID Count: 17

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (2)
W 402	Undefined organism found in <213> in SEQ ID (3)
W 402	Undefined organism found in <213> in SEQ ID (4)
W 402	Undefined organism found in <213> in SEQ ID (5)
W 402	Undefined organism found in <213> in SEQ ID (6)
W 402	Undefined organism found in <213> in SEQ ID (7)
W 402	Undefined organism found in <213> in SEQ ID (8)
W 402	Undefined organism found in <213> in SEQ ID (9)
W 402	Undefined organism found in <213> in SEQ ID (10)
W 402	Undefined organism found in <213> in SEQ ID (11)
W 402	Undefined organism found in <213> in SEQ ID (12)
W 402	Undefined organism found in <213> in SEQ ID (13)
W 402	Undefined organism found in <213> in SEQ ID (14)
W 402	Undefined organism found in <213> in SEQ ID (15)
W 402	Undefined organism found in <213> in SEQ ID (16)
W 402	Undefined organism found in <213> in SEQ ID (17)

SEQUENCE LISTING

<110> SUZUKI, Toshiharu et al.

<120> MARKER PEPTIDE FOR ALZHEIMER'S DISEASE

<130> 3749-0112PUS1

<140> 10577008

<141> 2006-08-07

<150> PCT/JP2004/016209

<151> 2004-11-01

<150> JP 2003/375363

<151> 2003-11-05

<160> 17

<170> PatentIn version 3.5

<210> 1

<211> 971

<212> PRT

<213> human

<400> 1

Met Leu Arg Arg Pro Ala Pro Ala Leu Ala Pro Ala Ala Arg Leu Leu

1	5	10	15
Leu Ala Gly Leu Leu Cys Gly Gly Gly Val Trp Ala Ala Arg Val Asn			
20	25	30	
Lys His Lys Pro Trp Leu Glu Pro Thr Tyr His Gly Ile Val Thr Glu			
35	40	45	
Asn Asp Asn Thr Val Leu Leu Asp Pro Pro Leu Ile Ala Leu Asp Lys			
50	55	60	
Asp Ala Pro Leu Arg Phe Ala Gly Glu Ile Cys Gly Phe Lys Ile His			
65	70	75	80
Gly Gln Asn Val Pro Phe Asp Ala Val Val Val Asp Lys Ser Thr Gly			
85	90	95	
Glu Gly Val Ile Arg Ser Lys Glu Lys Leu Asp Cys Glu Leu Gln Lys			
100	105	110	
Asp Tyr Ser Phe Thr Ile Gln Ala Tyr Asp Cys Gly Lys Gly Pro Asp			
115	120	125	

Gly Thr Asn Val Lys Lys Ser His Lys Ala Thr Val His Ile Gln Val

130

135

140

Asn Asp Val Asn Glu Tyr Ala Pro Val Phe Lys Glu Lys Ser Tyr Lys

145

150

155

160

Ala Thr Val Ile Glu Gly Lys Gln Tyr Asp Ser Ile Leu Arg Val Glu

165

170

175

Ala Val Asp Ala Asp Cys Ser Pro Gln Phe Ser Gln Ile Cys Ser Tyr

180

185

190

Glu Ile Ile Thr Pro Asp Val Pro Phe Thr Val Asp Lys Asp Gly Tyr

195

200

205

Ile Lys Asn Thr Glu Lys Leu Asn Tyr Gly Lys Glu His Gln Tyr Lys

210

215

220

Leu Thr Val Thr Ala Tyr Asp Cys Gly Lys Lys Arg Ala Thr Glu Asp

225

230

235

240

Val Leu Val Lys Ile Ser Ile Lys Pro Thr Cys Thr Pro Gly Trp Gln

245

250

255

Gly Trp Asn Asn Arg Ile Glu Tyr Glu Pro Gly Thr Gly Ala Leu Ala

260

265

270

Val Phe Pro Asn Ile His Leu Glu Thr Cys Asp Glu Pro Val Ala Ser

275

280

285

Val Gln Ala Thr Val Glu Leu Glu Thr Ser His Ile Gly Lys Gly Cys

290

295

300

Asp Arg Asp Thr Tyr Ser Glu Lys Ser Leu His Arg Leu Cys Gly Ala

305

310

315

320

Ala Ala Gly Thr Ala Glu Leu Leu Pro Ser Pro Ser Gly Ser Leu Asn

325

330

335

Trp Thr Met Gly Leu Pro Thr Asp Asn Gly His Asp Ser Asp Gln Val

340

345

350

Phe Glu Phe Asn Gly Thr Gln Ala Val Arg Ile Pro Asp Gly Val Val

355

360

365

Ser Val Ser Pro Lys Glu Pro Phe Thr Ile Ser Val Trp Met Arg His

370

375

380

Gly Pro Phe Gly Arg Lys Lys Glu Thr Ile Leu Cys Ser Ser Asp Lys

385

390

395

400

Thr Asp Met Asn Arg His His Tyr Ser Leu Tyr Val His Gly Cys Arg

405

410

415

Leu Ile Phe Leu Phe Arg Gln Asp Pro Ser Glu Glu Lys Lys Tyr Arg

420

425

430

Pro Ala Glu Phe His Trp Lys Leu Asn Gln Val Cys Asp Glu Glu Trp

435

440

445

His His Tyr Val Leu Asn Val Glu Phe Pro Ser Val Thr Leu Tyr Val

450

455

460

Asp Gly Thr Ser His Glu Pro Phe Ser Val Thr Glu Asp Tyr Pro Leu

465 470 475 480

His Pro Ser Lys Ile Glu Thr Gln Leu Val Val Gly Ala Cys Trp Gln

485 490 495

Glu Phe Ser Gly Val Glu Asn Asp Asn Glu Thr Glu Pro Val Thr Val

500 505 510

Ala Ser Ala Gly Gly Asp Leu His Met Thr Gln Phe Phe Arg Gly Asn

515 520 525

Leu Ala Gly Leu Thr Leu Arg Ser Gly Lys Leu Ala Asp Lys Lys Val

530 535 540

Ile Asp Cys Leu Tyr Thr Cys Lys Glu Gly Leu Asp Leu Gln Val Leu

545 550 555 560

Glu Asp Ser Gly Arg Gly Val Gln Ile Gln Ala His Pro Ser Gln Leu

565 570 575

Val Leu Thr Leu Glu Gly Glu Asp Leu Gly Glu Leu Asp Lys Ala Met

580

585

590

Gln His Ile Ser Tyr Leu Asn Ser Arg Gln Phe Pro Thr Pro Gly Ile

595

600

605

Arg Arg Leu Lys Ile Thr Ser Thr Ile Lys Cys Phe Asn Glu Ala Thr

610

615

620

Cys Ile Ser Val Pro Pro Val Asp Gly Tyr Val Met Val Leu Gln Pro

625

630

635

640

Glu Glu Pro Lys Ile Ser Leu Ser Gly Val His His Phe Ala Arg Ala

645

650

655

Ala Ser Glu Phe Glu Ser Ser Glu Gly Val Phe Leu Phe Pro Glu Leu

660

665

670

Arg Ile Ile Ser Thr Ile Thr Arg Glu Val Glu Pro Glu Gly Asp Gly

675

680

685

Ala Glu Asp Pro Thr Val Gln Glu Ser Leu Val Ser Glu Glu Ile Val

690

695

700

His Asp Leu Asp Thr Cys Glu Val Thr Val Glu Gly Glu Glu Leu Asn

705

710

715

720

His Glu Gln Glu Ser Leu Glu Val Asp Met Ala Arg Leu Gln Gln Lys

725

730

735

Gly Ile Glu Val Ser Ser Ser Glu Leu Gly Met Thr Phe Thr Gly Val

740

745

750

Asp Thr Met Ala Ser Tyr Glu Glu Val Leu His Leu Leu Arg Tyr Arg

755

760

765

Asn Trp His Ala Arg Ser Leu Leu Asp Arg Lys Phe Lys Leu Ile Cys

770

775

780

Ser Glu Leu Asn Gly Arg Tyr Ile Ser Asn Glu Phe Lys Val Glu Val

785

790

795

800

Asn Val Ile His Thr Ala Asn Pro Met Glu His Ala Asn His Met Ala

805

810

815

Ala Gln Pro Gln Phe Val His Pro Glu His Arg Ser Phe Val Asp Leu

820

825

830

Ser Gly His Asn Leu Ala Asn Pro His Pro Phe Ala Val Val Pro Ser

835

840

845

Thr Ala Thr Val Val Ile Val Val Cys Val Ser Phe Leu Val Phe Met

850

855

860

Ile Ile Leu Gly Val Phe Arg Ile Arg Ala Ala His Arg Arg Thr Met

865

870

875

880

Arg Asp Gln Asp Thr Gly Lys Glu Asn Glu Met Asp Trp Asp Asp Ser

885

890

895

Ala Leu Thr Ile Thr Val Asn Pro Met Glu Thr Tyr Glu Asp Gln His

900

905

910

Ser Ser Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Ser Glu Asp

915

920

925

Gly Glu Glu Glu Asp Asp Ile Thr Ser Ala Glu Ser Glu Ser Ser Glu

930

935

940

Glu Glu Glu Gly Glu Gln Gly Asp Pro Gln Asn Ala Thr Arg Gln Gln

945

950

955

960

Gln Leu Glu Trp Asp Asp Ser Thr Leu Ser Tyr

965

970

<210> 2

<211> 968

<212> PRT

<213> human

<400> 2

Met Val Leu Gly Cys Glu Leu Ser Gly Ser Thr Arg Val Val Val Gly

1

5

10

15

Val Glu Ala Leu Leu Thr Gly Ala Ser Ser Pro Leu Pro Gly Val Gly

20

25

30

Pro Ala Asn Lys His Lys Pro Trp Ile Glu Ala Glu Tyr Gln Gly Ile

35

40

45

Val Met Glu Asn Asp Asn Thr Val Leu Leu Asn Pro Pro Leu Phe Ala

50

55

60

Leu Asp Lys Asp Ala Pro Leu Arg Tyr Ala Gly Glu Ile Cys Gly Phe

65

70

75

80

Arg Leu His Gly Ser Gly Val Pro Phe Glu Ala Val Ile Leu Asp Lys

85

90

95

Ala Thr Gly Glu Gly Leu Ile Arg Ala Lys Glu Pro Val Asp Cys Glu

100

105

110

Ala Gln Lys Glu His Thr Phe Thr Ile Gln Ala Tyr Asp Cys Gly Glu

115

120

125

Gly Pro Asp Gly Ala Asn Thr Lys Lys Ser His Lys Ala Thr Val His

130

135

140

Val Arg Val Asn Asp Val Asn Glu Phe Ala Pro Val Phe Val Glu Arg

145 150 155 160

Leu Tyr Arg Ala Ala Val Thr Glu Gly Lys Leu Tyr Asp Arg Ile Leu

165 170 175

Arg Val Glu Ala Ile Asp Gly Asp Cys Ser Pro Gln Tyr Ser Gln Ile

180 185 190

Cys Tyr Tyr Glu Ile Leu Thr Pro Asn Thr Pro Phe Leu Ile Asp Asn

195 200 205

Asp Gly Asn Ile Glu Asn Thr Glu Lys Leu Gln Tyr Ser Gly Glu Arg

210 215 220

Leu Tyr Lys Phe Thr Val Thr Ala Tyr Asp Cys Gly Lys Lys Arg Ala

225 230 235 240

Ala Asp Asp Ala Glu Val Glu Ile Gln Val Lys Pro Thr Cys Lys Pro

245 250 255

Ser Trp Gln Gly Trp Asn Lys Arg Ile Glu Tyr Ala Pro Gly Ala Gly

260

265

270

Ser Leu Ala Leu Phe Pro Gly Ile Arg Leu Glu Thr Cys Asp Glu Pro

275

280

285

Leu Trp Asn Ile Gln Ala Thr Ile Glu Leu Gln Thr Ser His Val Ala

290

295

300

Lys Gly Cys Asp Arg Asp Asn Tyr Ser Glu Arg Ala Leu Arg Lys Leu

305

310

315

320

Cys Gly Ala Ala Thr Gly Glu Val Asp Leu Leu Pro Met Pro Gly Pro

325

330

335

Asn Ala Asn Trp Thr Ala Gly Leu Ser Val His Tyr Ser Gln Asp Ser

340

345

350

Ser Leu Ile Tyr Trp Phe Asn Gly Thr Gln Ala Val Gln Val Pro Leu

355

360

365

Gly Gly Pro Ser Gly Leu Gly Ser Gly Pro Gln Asp Ser Leu Ser Asp

370

375

380

His Phe Thr Leu Ser Phe Trp Met Lys His Gly Val Thr Pro Asn Lys

385

390

395

400

Gly Lys Lys Glu Glu Glu Thr Ile Val Cys Asn Thr Val Gln Asn Glu

405

410

415

Asp Gly Phe Ser His Tyr Ser Leu Thr Val His Gly Cys Arg Ile Ala

420

425

430

Phe Leu Tyr Trp Pro Leu Leu Glu Ser Ala Arg Pro Val Lys Phe Leu

435

440

445

Trp Lys Leu Glu Gln Val Cys Asp Asp Glu Trp His His Tyr Ala Leu

450

455

460

Asn Leu Glu Phe Pro Thr Val Thr Leu Tyr Thr Asp Gly Ile Ser Phe

465

470

475

480

Asp Pro Ala Leu Ile His Asp Asn Gly Leu Ile His Pro Pro Arg Arg

485

490

495

Glu Pro Ala Leu Met Ile Gly Ala Cys Trp Thr Glu Glu Lys Asn Lys

500

505

510

Glu Lys Glu Lys Gly Asp Asn Ser Thr Asp Thr Thr Gln Gly Asp Pro

515

520

525

Leu Ser Ile His His Tyr Phe His Gly Tyr Leu Ala Gly Phe Ser Val

530

535

540

Arg Ser Gly Arg Leu Glu Ser Arg Glu Val Ile Glu Cys Leu Tyr Ala

545

550

555

560

Cys Arg Glu Gly Leu Asp Tyr Arg Asp Phe Glu Ser Leu Gly Lys Gly

565

570

575

Met Lys Val His Val Asn Pro Ser Gln Ser Leu Leu Thr Leu Glu Gly

580

585

590

Asp Asp Val Glu Thr Phe Asn His Ala Leu Gln His Val Ala Tyr Met

595

600

605

Asn Thr Leu Arg Phe Ala Thr Pro Gly Val Arg Pro Leu Arg Leu Thr

610

615

620

Thr Ala Val Lys Cys Phe Ser Glu Glu Ser Cys Val Ser Ile Pro Glu

625

630

635

640

Val Glu Gly Tyr Val Val Val Leu Gln Pro Asp Ala Pro Gln Ile Leu

645

650

655

Leu Ser Gly Thr Ala His Phe Ala Arg Pro Ala Val Asp Phe Glu Gly

660

665

670

Thr Asn Gly Val Pro Leu Phe Pro Asp Leu Gln Ile Thr Cys Ser Ile

675

680

685

Ser His Gln Val Glu Ala Lys Lys Asp Glu Ser Trp Gln Gly Thr Val

690

695

700

Thr Asp Thr Arg Met Ser Asp Glu Ile Val His Asn Leu Asp Gly Cys

705

710

715

720

Glu Ile Ser Leu Val Gly Asp Asp Leu Asp Pro Glu Arg Glu Ser Leu

725

730

735

Leu Leu Asp Thr Thr Ser Leu Gln Gln Arg Gly Leu Glu Leu Thr Asn

740

745

750

Thr Ser Ala Tyr Leu Thr Ile Ala Gly Val Glu Ser Ile Thr Val Tyr

755

760

765

Glu Glu Ile Leu Arg Gln Ala Arg Tyr Arg Leu Arg His Gly Ala Ala

770

775

780

Leu Tyr Thr Arg Lys Phe Arg Leu Ser Cys Ser Glu Met Asn Gly Arg

785

790

795

800

Tyr Ser Ser Asn Glu Phe Ile Val Glu Val Asn Val Leu His Ser Met

805

810

815

Asn Arg Val Ala His Pro Ser His Val Leu Ser Ser Gln Gln Phe Leu

820

825

830

His Arg Gly His Gln Pro Pro Pro Glu Met Ala Gly His Ser Leu Ala

835

840

845

Ser Ser His Arg Asn Ser Met Ile Pro Ser Ala Ala Thr Leu Ile Ile

850

855

860

Val Val Cys Val Gly Phe Leu Val Leu Met Val Val Leu Gly Leu Val

865

870

875

880

Arg Ile His Ser Leu His Arg Arg Val Ser Gly Ala Gly Gly Pro Pro

885

890

895

Gly Ala Ser Ser Asp Pro Lys Asp Pro Asp Leu Phe Trp Asp Asp Ser

900

905

910

Ala Leu Thr Ile Ile Val Asn Pro Met Glu Ser Tyr Gln Asn Arg Gln

915

920

925

Ser Cys Val Thr Gly Ala Val Gly Gly Gln Gln Glu Asp Glu Asp Ser

930

935

940

Ser Asp Ser Glu Val Ala Asp Ser Pro Ser Ser Asp Glu Arg Arg Ile

945

950

955

960

Ile Glu Thr Pro Pro His Arg Tyr

965

<210> 3

<211> 955

<212> PRT

<213> human

<400> 3

Met Leu Pro Gly Arg Leu Cys Trp Val Pro Leu Leu Leu Ala Leu Gly

1

5

10

15

Val Gly Ser Gly Ser Gly Gly Gly Gly Asp Ser Arg Gln Arg Arg Leu

20